

## SEQUENCE LISTING

&lt;110&gt; AKZO Nobel N.V.

<120> *Lawsonia intracellularis* subunit vaccines.

&lt;130&gt; 2004.001

&lt;160&gt; 18

&lt;170&gt; PatentIn version 3.2

&lt;210&gt; 1

&lt;211&gt; 2088

&lt;212&gt; DNA

<213> *Lawsonia intracellularis*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (16)..(2085)

&lt;400&gt; 1

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gct aac gta aat aca gta ggc ttt aaa ggc caa cgt atg gat ttc gca      147
Ala Asn Val Asn Thr Val Gly Phe Lys Gly Gln Arg Met Asp Phe Ala
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Asp Phe Ile Tyr Gln Asp Gly Phe Ser Thr Ala Gly Ile Thr Gln Ile
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gga cgt ggt gta ggc att gga gct gtc atg ggg aac ttt ggt cag ggt      243
Gly Arg Gly Val Gly Ile Gly Ala Val Met Gly Asn Phe Gly Gln Gly
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Gly Phe Phe Lys Val Lys Pro Gln Gly Ser Glu Thr Ser Tyr Tyr Thr
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Arg Ala Gly Asn Phe Arg Phe Asn Asn Asp Gly Tyr Leu Val Asp Pro
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cat gga tat gct ctt cag ggt tgg aaa att gat aat act gaa ggg cca      435
His Gly Tyr Ala Leu Gln Gly Trp Lys Ile Asp Asn Thr Glu Gly Pro
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Asp Lys Ser Gly Asp Lys Ser Gln Asn Val Asn Ser Pro Phe Thr Ser	
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Pro Met Pro Glu Ser Ala Tyr Ser Tyr Gln Thr Ser Ile Lys Val Tyr	
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Asp Glu Ala Gly Thr His Thr Leu Thr Val Tyr Phe Asp Gln Val	
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Ser Pro Lys Asp Tyr Lys Gly Gly Gly Ser Gly Glu Ser Val Trp Glu	
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Gln Asp Gly Phe Ser Thr Ala Gly Ile Thr Gln Ile Gly Arg Gly Val  
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Gly Ile Gly Ala Val Met Gly Asn Phe Gly Gln Gly Ser Phe Glu Thr  
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Thr Thr Glu Ala Thr Asp Leu Ala Ile Gly Gly Arg Gly Phe Phe Lys  
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Val Lys Pro Gln Gly Ser Glu Thr Ser Tyr Tyr Thr Arg Ala Gly Asn  
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Phe Arg Phe Asn Asn Asp Gly Tyr Leu Val Asp Pro His Gly Tyr Ala  
 115 120 125

Leu Gln Gly Trp Lys Ile Asp Asn Thr Glu Gly Pro Gln Arg Ile Ser  
 130 135 140

Gly Gly Val Asn Pro Gly Thr Asn Thr Ser Gln Ile Met Gly Thr Gly  
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Glu Pro Thr Asp Ile Arg Leu Asp Thr Trp Thr Val Ala Pro Leu Gln  
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Thr Thr Asn Val Ser Phe Asn Val Asn Leu Ser Ser Asp Lys Ser Gly  
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Asp Lys Ser Gln Asn Val Asn Ser Pro Phe Thr Ser Leu Phe Asn Ile  
195 200 205

Trp Asn Gly Lys Gln Pro Ser Glu Pro Asn Asn Pro Pro Met Pro Glu  
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Ser Ala Tyr Ser Tyr Gln Thr Ser Ile Lys Val Tyr Asp Glu Ala Gly  
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Gly Thr His Thr Leu Thr Val Tyr Phe Asp Gln Val Ser Pro Lys Asp  
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Tyr Lys Gly Gly Gly Ser Gly Glu Ser Val Trp Glu Tyr Val Val Thr  
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Met Asp Pro Ser Glu Asp Asn Arg Gln Val Ser Val Gly Gly Asn Ile  
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Val Asp Ile Lys Asp Thr Lys Ala Ala Gly Met Leu Met Ser Gly Thr  
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Gly Lys Asn Thr Ala Gly Ser Val Gly Asp Ala Thr Thr Phe Phe Thr  
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Glu Ile Asp Phe Gly Leu Lys Ala Thr Asp Leu Asp Asn Thr Trp Lys  
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Ala Pro Ser Val Thr Glu Leu Gly Met Ala Gln Ile Leu Glu Asn Pro

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 Ala Gly Val Met Pro Gln Tyr Tyr Phe Gly Asn Pro Asn Tyr Asp Asn  
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 Thr Val Pro Gln Ser Pro Pro Tyr Val Tyr Lys Asn Glu Ala Ser Tyr  
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 Glu Ala Asn Asp Pro Pro Asn Val Lys Asp Leu Ala Asn Met Asn Gly  
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 Thr Pro Asn Arg Leu Ser Asn Ala Phe Thr Asn Tyr Ala Gly Gly Ser  
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 Ser Thr Lys Ser Ala Ser Gln Asn Gly Tyr Gly Phe Gly Asp Leu Met  
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 Gly Val Gln Leu Pro Leu Tyr Gln Val Ala Leu Tyr Asp Phe Asn Ser  
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 Lys Gln Gly Leu Arg Arg Glu Gly Gly Asn Leu Phe Ser Gln Thr Arg  
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 Glu Ser Gly Asp Pro Ser Ser Gly Ala Ala Asn Thr Ser Gly Phe Gly  
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&lt;212&gt; DNA

<213> *Lawsonia intracellularis*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (32)..(715)

&lt;400&gt; 3

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Phe Thr Val Gly Ile Ile Met Leu Ile Leu Ala Cys Leu Ala Ala Leu
          10                               15                               20

gag ttc ata caa gat ttt ccc aat agc tat caa gaa gat gga caa atg      148
Glu Phe Ile Gln Asp Phe Pro Asn Ser Tyr Gln Glu Asp Gly Gln Met
          25                               30                               35

gtt aca gga att att tca aaa ata ata ggc tct aac tgt gat aat tct      196
Val Thr Gly Ile Ile Ser Lys Ile Ile Gly Ser Asn Cys Asp Asn Ser
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tca aca tct gat ata aat aat aag aaa tcc ata gat aga gat aaa gat      244
Ser Thr Ser Asp Ile Asn Asn Lys Lys Ser Ile Asp Arg Asp Lys Asp
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aca tta ctc tca agt agt aat aga aat aca ata caa gcc ggt act cca      292
Thr Leu Leu Ser Ser Ser Asn Arg Asn Thr Ile Gln Ala Gly Thr Pro
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cat caa gaa aat aac ata aaa gaa gat ctt caa ctg act aac aaa aat      340
His Gln Glu Asn Asn Ile Lys Glu Asp Leu Gln Leu Thr Asn Lys Asn
          90                               95                               100

gaa caa aca act cca gaa gaa gaa gaa gaa agt aaa ttt att tgg tta      388
Glu Gln Thr Thr Pro Glu Glu Glu Glu Glu Ser Lys Phe Ile Trp Leu
          105                               110                               115

aca gaa gct cca tca gag ctt aaa aaa gga gaa aaa gct ata aca caa      436
Thr Glu Ala Pro Ser Glu Leu Lys Lys Gly Glu Lys Ala Ile Thr Gln
          120                               125                               130                               135

aca aga ttg tct att ggt aag gat ata tct ttt aga att act gct gat      484
Thr Arg Leu Ser Ile Gly Lys Asp Ile Ser Phe Arg Ile Thr Ala Asp
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gat gcc atc aaa gct caa tca atg atg tta aaa aat cca gat agg ttt      532
Asp Ala Ile Lys Ala Gln Ser Met Met Leu Lys Asn Pro Asp Arg Phe
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gtt tta gat ctt caa gga aag tgg ggt att tcc ctt cca cct att cca      580
Val Leu Asp Leu Gln Gly Lys Trp Gly Ile Ser Leu Pro Pro Ile Pro
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cct aca aat cct tgg tta aaa aaa ata cgc tta ggt act aat aat gga      628
Pro Thr Asn Pro Trp Leu Lys Lys Ile Arg Leu Gly Thr Asn Asn Gly
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Tyr Gln Glu Asp Gly Gln Met Val Thr Gly Ile Ile Ser Lys Ile Ile  
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Gly Ser Asn Cys Asp Asn Ser Ser Thr Ser Asp Ile Asn Asn Lys Lys  
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Ser Ile Asp Arg Asp Lys Asp Thr Leu Leu Ser Ser Ser Asn Arg Asn  
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Thr Ile Gln Ala Gly Thr Pro His Gln Glu Asn Asn Ile Lys Glu Asp  
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Leu Gln Leu Thr Asn Lys Asn Glu Gln Thr Thr Pro Glu Glu Glu Glu  
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Glu Ser Lys Phe Ile Trp Leu Thr Glu Ala Pro Ser Glu Leu Lys Lys  
 115 120 125

Gly Glu Lys Ala Ile Thr Gln Thr Arg Leu Ser Ile Gly Lys Asp Ile  
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Ser Phe Arg Ile Thr Ala Asp Asp Ala Ile Lys Ala Gln Ser Met Met  
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Leu Lys Asn Pro Asp Arg Phe Val Leu Asp Leu Gln Gly Lys Trp Gly  
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Ile Ser Leu Pro Pro Ile Pro Pro Thr Asn Pro Trp Leu Lys Lys Ile  
 180 185 190

Arg Leu Gly Thr Asn Asn Gly Asn Thr Arg Leu Val Phe Asp Leu Gln  
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Lys Lys Pro Ser Lys Thr Glu Ile Lys Gln Leu Asp Thr Asn Lys Ile  
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 <222> (34)..(1677)

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ctt tat tgg gaa gaa cgt ttt caa cct atc ccg gat gct aat gct att 246  
 Leu Tyr Trp Glu Glu Arg Phe Gln Pro Ile Pro Asp Ala Asn Ala Ile  
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aaa gca gga aag gta gaa gat ata aag gaa atg gat aag gca agg ata 294  
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 75 80 85

gct aca ggt gca gac tat ctt ata tgg gga cag gta aat att gta ggt 342  
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gat gaa gct acg ctt gat gta caa gtt tgt gat ata gaa gga tca att 390  
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 105 110 115

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 120 125 130 135

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 140 145 150

aca aaa cca tca tca aaa gct act att gta gct caa atg aac tct gga 534  
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 155 160 165

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Phe	Arg	Tyr	Gln	Gly	Ser	Asn	Leu	Ser	Arg	Gly	Arg	Ser	Gln	Ala	Leu	
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ccc	ttt	gct	tca	gtt	ggc	ata	gtt	gtt	ggc	gac	ttt	ata	gga	gat	aat	678
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Lys	Asn	Glu	Val	Ala	Ile	Leu	Ser	Glu	Tyr	Lys	Val	His	Ile	Tyr	Arg	
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Trp	Glu	Glu	Glu	Arg	Leu	Ala	Leu	Leu	Gly	Glu	Tyr	Lys	Phe	Pro	Arg	
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Ser	Leu	Gln	Ser	Leu	His	Ile	Arg	Ala	Phe	Asp	Val	Asp	His	Asp	Gly	
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Val	Gln	Glu	Ile	Ile	Val	Ser	Cys	Phe	Asp	Pro	Ser	Tyr	Ala	Lys	Pro	
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Tyr	Ser	Phe	Ile	Leu	Ser	Phe	Lys	Asn	Arg	Val	Phe	Lys	Glu	Leu	Ala	
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Pro	Ser	Gly	Val	Tyr	Glu	Ile	Glu	Lys	His	Gly	Arg	Asn	Tyr	Ile	Met	
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Gly	Asn	Arg	Leu	Ser	Leu	Pro	Lys	Glu	Ala	Asn	Ile	Phe	Asn	Phe	Ser	
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Trp	Leu	Pro	Ser	Asp	Ser	Leu	Lys	Asp	Glu	Glu	Ala	Lys	Leu	Val	Leu	
360					365				370						375	
gta	acc	aat	aat	gaa	aga	tta	gtt	gta	tat	aat	aca	aaa	ggc	aca	aga	1206
Val	Thr	Asn	Asn	Glu	Arg	Leu	Val	Val	Tyr	Asn	Thr	Lys	Gly	Thr	Arg	
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ctt	ttt	atg	act	gaa	gaa	gtg	tat	tat	ggc	tct	tct	gtt	ggc	ata	gac	1254
Leu	Phe	Met	Thr	Glu	Glu	Val	Tyr	Tyr	Gly	Ser	Ser	Val	Gly	Ile	Asp	
			395					400					405			
gag	ccc	agt	aat	atg	cct	ggc	ctt	gga	aag	tca	aaa	gag	ctt	atc	cct	1302
Glu	Pro	Ser	Asn	Met	Pro	Gly	Leu	Gly	Lys	Ser	Lys	Glu	Leu	Ile	Pro	
		410					415					420				
tct	aaa	tat	ttt	atc	cca	gga	cgg	atg	att	cct	att	aat	ctt	gat	tca	1350
Ser	Lys	Tyr	Phe	Ile	Pro	Gly	Arg	Met	Ile	Pro	Ile	Asn	Leu	Asp	Ser	

425 430 435

atg ggg aaa tgg gag ttg ctt gta agc aag cca att tct gtt gca gca 1398  
 Met Gly Lys Trp Glu Leu Leu Val Ser Lys Pro Ile Ser Val Ala Ala  
 440 445 450 455

aaa ttt ttt gaa aat tat aga tct ttt gct gaa ggc gaa att cag gct 1446  
 Lys Phe Phe Glu Asn Tyr Arg Ser Phe Ala Glu Gly Glu Ile Gln Ala  
 460 465 470

tta aca tgg gac ggc tta gga tta ggt ctt gta tgg aat aca cgt cgt 1494  
 Leu Thr Trp Asp Gly Leu Gly Leu Gly Leu Val Trp Asn Thr Arg Arg  
 475 480 485

att aag gga act att aca gat ttt gcc tta gct gat atg aat aat gat 1542  
 Ile Lys Gly Thr Ile Thr Asp Phe Ala Leu Ala Asp Met Asn Asn Asp  
 490 495 500

ggg aag tta gac tta gtt gtt tcc gtt aat agc cat aca ggg att ctt 1590  
 Gly Lys Leu Asp Leu Val Ser Val Asn Ser His Thr Gly Ile Leu  
 505 510 515

gga cta gaa aaa cga aag aca att ata gta ttt tat cct tta gag gta 1638  
 Gly Leu Glu Lys Arg Lys Thr Ile Ile Val Phe Tyr Pro Leu Glu Val  
 520 525 530 535

gat aaa caa ggt atc cct aag gct gtt gaa gat aac taa ttttttccta 1687  
 Asp Lys Gln Gly Ile Pro Lys Ala Val Glu Asp Asn  
 540 545

ttaattattt ttttattctg atagttaa 1715

<210> 6  
 <211> 547  
 <212> PRT  
 <213> Lawsonia intracellularis

<400> 6

Met His Gln Lys Ser Cys Leu Val Ala Leu Cys Ile Met Phe Ile Ile  
 1 5 10 15

Met Val Gln Val Leu Gln Ala Asn Ala Ala Ser Tyr Val Val Leu Pro  
 20 25 30

Phe Lys Val Asn Ala Pro Pro Ser Tyr Thr Tyr Leu Glu Lys Ala Ile  
 35 40 45

Pro Ser Met Leu Thr Ser Arg Leu Tyr Trp Glu Glu Arg Phe Gln Pro  
 50 55 60

Ile Pro Asp Ala Asn Ala Ile Lys Ala Gly Lys Val Glu Asp Ile Lys  
 65 70 75 80

Glu Met Asp Lys Ala Arg Ile Ala Thr Gly Ala Asp Tyr Leu Ile Trp  
 85 90 95

Gly Gln Val Asn Ile Val Gly Asp Glu Ala Thr Leu Asp Val Gln Val

100	105	110
Cys Asp Ile Glu Gly Ser Ile Trp Arg Lys Ser Lys Asn Thr Lys Val 115 120 125		
Asp Asn Leu Ile Thr Ala Leu Gln Asp Thr Ala Asp Ala Ile Asn Ser 130 135 140		
Glu Leu Phe Gly Arg Ala Thr Thr Lys Pro Ser Ser Lys Ala Thr Ile 145 150 155 160		
Val Ala Gln Met Asn Ser Gly Leu Ile Lys Gly Lys Gly Asn Glu Asn 165 170 175		
Gln Ser Tyr Leu Asn Pro Glu Phe Arg Tyr Gln Gly Ser Asn Leu Ser 180 185 190		
Arg Gly Arg Ser Gln Ala Leu Pro Phe Ala Ser Val Gly Ile Val Val 195 200 205		
Gly Asp Phe Ile Gly Asp Asn Lys Asn Glu Val Ala Ile Leu Ser Glu 210 215 220		
Tyr Lys Val His Ile Tyr Arg Trp Glu Glu Glu Arg Leu Ala Leu Leu 225 230 235 240		
Gly Glu Tyr Lys Phe Pro Arg Ser Leu Gln Ser Leu His Ile Arg Ala 245 250 255		
Phe Asp Val Asp His Asp Gly Val Gln Glu Ile Ile Val Ser Cys Phe 260 265 270		
Asp Pro Ser Tyr Ala Lys Pro Tyr Ser Phe Ile Leu Ser Phe Lys Asn 275 280 285		
Arg Val Phe Lys Glu Leu Ala Thr Asn Leu Pro Phe Tyr Leu Asn Val 290 295 300		
Val Lys Leu Pro Pro Asp Phe Ser Pro Met Leu Ile Gly Gln Lys Ser 305 310 315 320		
Asp Asn Ser Arg Ile Phe Ser Pro Ser Gly Val Tyr Glu Ile Glu Lys 325 330 335		
His Gly Arg Asn Tyr Ile Met Gly Asn Arg Leu Ser Leu Pro Lys Glu 340 345 350		
Ala Asn Ile Phe Asn Phe Ser Trp Leu Pro Ser Asp Ser Leu Lys Asp 355 360 365		

Glu Glu Ala Lys Leu Val Leu Val Thr Asn Asn Glu Arg Leu Val Val  
370 375 380

Tyr Asn Thr Lys Gly Thr Arg Leu Phe Met Thr Glu Glu Val Tyr Tyr  
385 390 395 400

Gly Ser Ser Val Gly Ile Asp Glu Pro Ser Asn Met Pro Gly Leu Gly  
405 410 415

Lys Ser Lys Glu Leu Ile Pro Ser Lys Tyr Phe Ile Pro Gly Arg Met  
420 425 430

Ile Pro Ile Asn Leu Asp Ser Met Gly Lys Trp Glu Leu Leu Val Ser  
435 440 445

Lys Pro Ile Ser Val Ala Ala Lys Phe Phe Glu Asn Tyr Arg Ser Phe  
450 455 460

Ala Glu Gly Glu Ile Gln Ala Leu Thr Trp Asp Gly Leu Gly Leu Gly  
465 470 475 480

Leu Val Trp Asn Thr Arg Arg Ile Lys Gly Thr Ile Thr Asp Phe Ala  
485 490 495

Leu Ala Asp Met Asn Asn Asp Gly Lys Leu Asp Leu Val Val Ser Val  
500 505 510

Asn Ser His Thr Gly Ile Leu Gly Leu Glu Lys Arg Lys Thr Ile Ile  
515 520 525

Val Phe Tyr Pro Leu Glu Val Asp Lys Gln Gly Ile Pro Lys Ala Val  
530 535 540

Glu Asp Asn  
545

<210> 7  
<211> 1564  
<212> DNA  
<213> Lawsonia intracellularis

<220>  
<221> CDS  
<222> (41)..(1522)

<400> 7  
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Met Val Ser Tyr Ile  
1 5

cgt tta tta gga agt ata ttt tta gta tta gca att ttt ggt tgt ggc Arg Leu Leu Gly Ser Ile Phe Leu Val Leu Ala Ile Phe Gly Cys Gly 10 15 20	103
gct cag ttt aat aaa ccc tct tta ctt gat gaa acc cct ata gat tac Ala Gln Phe Asn Lys Pro Ser Leu Leu Asp Glu Thr Pro Ile Asp Tyr 25 30 35	151
agt tct gta ctt tct gat tac ata gta gaa tta gaa aaa gaa cca ctt Ser Ser Val Leu Ser Asp Tyr Ile Val Glu Leu Glu Lys Glu Pro Leu 40 45 50	199
cag tat ata tta cta aaa aaa gaa aaa ttt tct caa atg gag ata tat Gln Tyr Ile Leu Leu Lys Lys Glu Lys Phe Ser Gln Met Glu Ile Tyr 55 60 65	247
aat tat caa ttc aca tca caa cat tgg tct cca gat aat ttt gta tca Asn Tyr Gln Phe Thr Ser Gln His Trp Ser Pro Asp Asn Phe Val Ser 70 75 80 85	295
cct gct ata tgg gaa cat cag gta gat ata tat atc cct cac cat cca Pro Ala Ile Trp Glu His Gln Val Asp Ile Tyr Ile Pro His His Pro 90 95 100	343
gtt tca gaa cgt gca ctt ctt atc atc aat aat ggt att aat aat ggt Val Ser Glu Arg Ala Leu Leu Ile Ile Asn Asn Gly Ile Asn Asn Gly 105 110 115	391
aca ttt ttt act tct cct aaa gct cca act gat ttt act cca gaa gta Thr Phe Phe Thr Ser Pro Lys Ala Pro Thr Asp Phe Thr Pro Glu Val 120 125 130	439
tta gaa gaa atc gct cgt tca aca aaa act gta gtc att gct cta agt Leu Glu Glu Ile Ala Arg Ser Thr Lys Thr Val Val Ile Ala Leu Ser 135 140 145	487
gat atc cca aat cag tat ctt act tat aga ggt gac tgg aga ttt ctt Asp Ile Pro Asn Gln Tyr Leu Thr Tyr Arg Gly Asp Trp Arg Phe Leu 150 155 160 165	535
aag gaa gat gaa agt att gct atg agt tgg tct agt ttt tta caa gat Lys Glu Asp Glu Ser Ile Ala Met Ser Trp Ser Ser Phe Leu Gln Asp 170 175 180	583
cca gaa agt cgg tac aca aga cct ctc tat gtc cct atg gtt gca gca Pro Glu Ser Arg Tyr Thr Arg Pro Leu Tyr Val Pro Met Val Ala Ala 185 190 195	631
gtt tct cag gca atg act ctt gca gaa aag gag tta caa gca tta aaa Val Ser Gln Ala Met Thr Leu Ala Glu Lys Glu Leu Gln Ala Leu Lys 200 205 210	679
att aag cat ttt att gta tct ggt gtg tca aag cgt gga tgg aca aca Ile Lys His Phe Ile Val Ser Gly Val Ser Lys Arg Gly Trp Thr Thr 215 220 225	727
tgg ctt tca gct att gct gac tca cga gta gat gct att acc ccg ttt Trp Leu Ser Ala Ile Ala Asp Ser Arg Val Asp Ala Ile Thr Pro Phe 230 235 240 245	775
gtt att gat gca ttg aat act cgg aaa gtc ctt gga cat atg tat aaa Val Ile Asp Ala Leu Asn Thr Arg Lys Val Leu Gly His Met Tyr Lys 250 255 260	823
aca tat gga aat aat tgg cct ata gca ttt tat cca tat tat aga ttt	871

Thr	Tyr	Gly	Asn	Asn	Trp	Pro	Ile	Ala	Phe	Tyr	Pro	Tyr	Tyr	Arg	Phe		
			265					270						275			
gat	tta	gat	aaa	caa	cta	gat	aca	ggt	cct	ttt	ttc	aat	ctt	atg	aat		919
Asp	Leu	Asp	Lys	Gln	Leu	Asp	Thr	Val	Pro	Phe	Phe	Asn	Leu	Met	Asn		
			280				285					290					
att	ggt	gat	cca	tat	aga	tat	tta	gga	aca	cca	tat	aag	tct	cga	ctt		967
Ile	Val	Asp	Pro	Tyr	Arg	Tyr	Leu	Gly	Thr	Pro	Tyr	Lys	Ser	Arg	Leu		
			295			300					305						
gct	atc	cct	aaa	tat	att	gta	aat	gca	agt	gga	gat	gat	ttt	tat	gtc		1015
Ala	Ile	Pro	Lys	Tyr	Ile	Val	Asn	Ala	Ser	Gly	Asp	Asp	Phe	Tyr	Val		
			310		315					320					325		
cct	gat	aat	tca	agt	ttt	tac	tat	gat	gat	ctc	cct	gga	gag	aaa	gca		1063
Pro	Asp	Asn	Ser	Ser	Phe	Tyr	Tyr	Asp	Asp	Leu	Pro	Gly	Glu	Lys	Ala		
				330				335						340			
tta	cgt	ttt	gca	cca	aac	tca	aat	cat	cat	ggg	ata	tta	aat	ttc	aca		1111
Leu	Arg	Phe	Ala	Pro	Asn	Ser	Asn	His	His	Gly	Ile	Leu	Asn	Phe	Thr		
			345					350					355				
aaa	caa	tcg	ctt	att	cct	ttt	gtg	aat	aga	gta	caa	aaa	ggg	att	tca		1159
Lys	Gln	Ser	Leu	Ile	Pro	Phe	Val	Asn	Arg	Val	Gln	Lys	Gly	Ile	Ser		
			360				365					370					
acg	cca	ggt	tta	gat	att	tcc	aca	gag	atg	acg	gaa	cga	ggt	caa	tat		1207
Thr	Pro	Val	Leu	Asp	Ile	Ser	Thr	Glu	Met	Thr	Glu	Arg	Val	Gln	Tyr		
						380					385						
gtg	act	ggt	cgt	ttt	tct	gaa	ggt	cca	gag	aag	ata	gta	ctt	tgg	aaa		1255
Val	Thr	Val	Arg	Phe	Ser	Glu	Val	Pro	Glu	Lys	Ile	Val	Leu	Trp	Lys		
					395					400					405		
gca	gca	aat	cca	gag	tca	cga	gat	ttt	cgt	tat	gcc	tgt	cgt	ggt	agg		1303
Ala	Ala	Asn	Pro	Glu	Ser	Arg	Asp	Phe	Arg	Tyr	Ala	Cys	Arg	Val	Arg		
				410				415						420			
tac	atg	gaa	aca	cca	tta	cac	ctt	tct	gca	aca	ggg	gaa	ggt	agc	ggt		1351
Tyr	Met	Glu	Thr	Pro	Leu	His	Leu	Ser	Ala	Thr	Gly	Glu	Val	Ser	Val		
				425				430					435				
tca	tta	gag	atc	cct	tct	gta	gga	tgg	caa	gct	gct	ttt	att	gaa	gct		1399
Ser	Leu	Glu	Ile	Pro	Ser	Val	Gly	Trp	Gln	Ala	Ala	Phe	Ile	Glu	Ala		
			440				445					450					
aca	ttt	aaa	gat	ggt	ttt	ggt	gca	aca	aca	cca	gtg	tat	att	tta	cca		1447
Thr	Phe	Lys	Asp	Gly	Phe	Val	Ala	Thr	Thr	Pro	Val	Tyr	Ile	Leu	Pro		
						460					465						
aaa	gat	ata	tat	cca	cct	ata	aaa	ata	cca	cct	gta	cat	gga	tta	tta		1495
Lys	Asp	Ile	Tyr	Pro	Pro	Ile	Lys	Ile	Pro	Pro	Val	His	Gly	Leu	Leu		
						475				480					485		
tgt	aag	ttt	gta	cat	ggt	cga	acc	tag	taactagtag	ttgttgtact							1542
Cys	Lys	Phe	Val	His	Gly	Arg	Thr										
						490											
gataatctaa	aaggatatag	at															1564

<210> 8  
 <211> 493  
 <212> PRT

&lt;213&gt; Lawsonia intracellularis

&lt;400&gt; 8

Met Val Ser Tyr Ile Arg Leu Leu Gly Ser Ile Phe Leu Val Leu Ala  
1 5 10 15

Ile Phe Gly Cys Gly Ala Gln Phe Asn Lys Pro Ser Leu Leu Asp Glu  
20 25 30

Thr Pro Ile Asp Tyr Ser Ser Val Leu Ser Asp Tyr Ile Val Glu Leu  
35 40 45

Glu Lys Glu Pro Leu Gln Tyr Ile Leu Leu Lys Lys Glu Lys Phe Ser  
50 55 60

Gln Met Glu Ile Tyr Asn Tyr Gln Phe Thr Ser Gln His Trp Ser Pro  
65 70 75 80

Asp Asn Phe Val Ser Pro Ala Ile Trp Glu His Gln Val Asp Ile Tyr  
85 90 95

Ile Pro His His Pro Val Ser Glu Arg Ala Leu Leu Ile Ile Asn Asn  
100 105 110

Gly Ile Asn Asn Gly Thr Phe Phe Thr Ser Pro Lys Ala Pro Thr Asp  
115 120 125

Phe Thr Pro Glu Val Leu Glu Glu Ile Ala Arg Ser Thr Lys Thr Val  
130 135 140

Val Ile Ala Leu Ser Asp Ile Pro Asn Gln Tyr Leu Thr Tyr Arg Gly  
145 150 155 160

Asp Trp Arg Phe Leu Lys Glu Asp Glu Ser Ile Ala Met Ser Trp Ser  
165 170 175

Ser Phe Leu Gln Asp Pro Glu Ser Arg Tyr Thr Arg Pro Leu Tyr Val  
180 185 190

Pro Met Val Ala Ala Val Ser Gln Ala Met Thr Leu Ala Glu Lys Glu  
195 200 205

Leu Gln Ala Leu Lys Ile Lys His Phe Ile Val Ser Gly Val Ser Lys  
210 215 220

Arg Gly Trp Thr Thr Trp Leu Ser Ala Ile Ala Asp Ser Arg Val Asp  
225 230 235 240

Ala Ile Thr Pro Phe Val Ile Asp Ala Leu Asn Thr Arg Lys Val Leu





<212> DNA  
 <213> *Lawsonia intracellularis*

<220>  
 <221> CDS  
 <222> (12)..(2096)

<400> 9  
 aggacaaaac t atg gcg gat tat ctt tca gga gga att tct ttt gga gga 50  
                   Met Ala Asp Tyr Leu Ser Gly Gly Ile Ser Phe Gly Gly  
                   1                  5                  10

att ggt agt gga acc gat ttc caa gct atg att gat caa ctt aag aaa 98  
 Ile Gly Ser Gly Thr Asp Phe Gln Ala Met Ile Asp Gln Leu Lys Lys  
           15                  20                  25

att gag ctt att cct aaa aat aga ctt gta gtt tcc cat gaa caa tgg 146  
 Ile Glu Leu Ile Pro Lys Asn Arg Leu Val Val Ser His Glu Gln Trp  
           30                  35                  40                  45

aca aaa aaa tat aaa gca ttt gaa gag ctt ata aaa aca gtt aaa gat 194  
 Thr Lys Lys Tyr Lys Ala Phe Glu Glu Leu Ile Lys Thr Val Lys Asp  
                   50                  55                  60

act gaa gcg tct tta agt aag cta agt tct gtt ggt gct att tta aaa 242  
 Thr Glu Ala Ser Leu Ser Lys Leu Ser Ser Val Gly Ala Ile Leu Lys  
                   65                  70                  75

aaa gaa ggt tct gtt tca aat act tct gtt gca agc gtt aag gca agt 290  
 Lys Glu Gly Ser Val Ser Asn Thr Ser Val Ala Ser Val Lys Ala Ser  
           80                  85                  90

tct gat gca tct gat gga aca cat aca att gat gtg aaa cag ctt gca 338  
 Ser Asp Ala Ser Asp Gly Thr His Thr Ile Asp Val Lys Gln Leu Ala  
           95                  100                  105

aca aac acg att ctt tct aat aat cat att ttt gat tct aaa act gaa 386  
 Thr Asn Thr Ile Leu Ser Asn Asn His Ile Phe Asp Ser Lys Thr Glu  
           110                  115                  120                  125

agt att aat aat aca ggt tca cct ggt atc ttt gct tat gag tat aaa 434  
 Ser Ile Asn Asn Thr Gly Ser Pro Gly Ile Phe Ala Tyr Glu Tyr Lys  
                   130                  135                  140

ggg gaa cta cat gaa gtt gaa gtt cct cca ggt agt gat ctt gaa tat 482  
 Gly Glu Leu His Glu Val Glu Val Pro Pro Gly Ser Asp Leu Glu Tyr  
                   145                  150                  155

ctt gca aca tta ata aac aaa gat tct aat aat cct ggt gtt aaa gca 530  
 Leu Ala Thr Leu Ile Asn Lys Asp Ser Asn Asn Pro Gly Val Lys Ala  
                   160                  165                  170

aac ctt atc aag act ggc gat ggc tat atg ttt agt ctt gaa gga act 578  
 Asn Leu Ile Lys Thr Gly Asp Gly Tyr Met Phe Ser Leu Glu Gly Thr  
           175                  180                  185

gaa act ggt gca aat gcg act tta tct att tca aat aag aca acg ctt 626  
 Glu Thr Gly Ala Asn Ala Thr Leu Ser Ile Ser Asn Lys Thr Thr Leu  
           190                  195                  200                  205

cca gac ttt aaa gca tct gtt gct acc agc agt gca tta gct aat ggt 674  
 Pro Asp Phe Lys Ala Ser Val Ala Thr Ser Ser Ala Leu Ala Asn Gly  
                   210                  215                  220

gaa gat aca att att aat act tca gga aca act caa caa ttt tct ttt	722
Glu Asp Thr Ile Ile Asn Thr Ser Gly Thr Thr Gln Gln Phe Ser Phe	
225 230 235	
gaa tac aat gga aga aca ttt act ttc gat att cct tca gga aca aca	770
Glu Tyr Asn Gly Arg Thr Phe Thr Phe Asp Ile Pro Ser Gly Thr Thr	
240 245 250	
gca aaa gaa ctc caa aca gct ata aat gaa aat aca aaa aat aca gga	818
Ala Lys Glu Leu Gln Thr Ala Ile Asn Glu Asn Thr Lys Asn Thr Gly	
255 260 265	
gta cgt gca act ttt gaa aaa cat ggc tca gat ata gta ttg caa tta	866
Val Arg Ala Thr Phe Glu Lys His Gly Ser Asp Ile Val Leu Gln Leu	
270 275 280 285	
gaa gga aca gtt cct aat caa caa gtt aaa gta acc gct agc cct act	914
Glu Gly Thr Val Pro Asn Gln Gln Val Lys Val Thr Ala Ser Pro Thr	
290 295 300	
gat ctt gga agt ttc aca tct tct ggt caa gca ggc tgg aat aaa cgt	962
Asp Leu Gly Ser Phe Thr Ser Ser Gly Gln Ala Gly Trp Asn Lys Arg	
305 310 315	
gat tct caa gat gct att ttt aat att aat ggt tgg gac caa gaa ctt	1010
Asp Ser Gln Asp Ala Ile Phe Asn Ile Asn Gly Trp Asp Gln Glu Leu	
320 325 330	
aca tct tct aca aat gaa ctt aca gaa gtt atc cca gga ctt caa att	1058
Thr Ser Ser Thr Asn Glu Leu Thr Glu Val Ile Pro Gly Leu Gln Ile	
335 340 345	
aca cta ctt tcc gaa ggg aaa aca caa att aca att cag act tct act	1106
Thr Leu Leu Ser Glu Gly Lys Thr Gln Ile Thr Ile Gln Thr Ser Thr	
350 355 360 365	
gac gaa gta aaa aaa caa gtt gag aaa gca gta gag tct ata aat aat	1154
Asp Glu Val Lys Lys Gln Val Glu Lys Ala Val Glu Ser Ile Asn Asn	
370 375 380	
gtt ctt tcc aaa att caa gag tta act aaa gca aca gct gaa gac aaa	1202
Val Leu Ser Lys Ile Gln Glu Leu Thr Lys Ala Thr Ala Glu Asp Lys	
385 390 395	
gat gat agt aaa gac act tct agt tct tca agt aaa att cca tca tat	1250
Asp Asp Ser Lys Asp Thr Ser Ser Ser Ser Ser Lys Ile Pro Ser Tyr	
400 405 410	
tta caa agt cct aca aaa gtg aag gct gga cta ttt aca ggt gat act	1298
Leu Gln Ser Pro Thr Lys Val Lys Ala Gly Leu Phe Thr Gly Asp Thr	
415 420 425	
ggc ata caa atg ctt agt act aga ctt aag tct atc ttt tct tct aat	1346
Gly Ile Gln Met Leu Ser Thr Arg Leu Lys Ser Ile Phe Ser Ser Asn	
430 435 440 445	
ggg cta ggt ttt tct cct aaa caa aca caa gat ggt cca ggg gat cta	1394
Gly Leu Gly Phe Ser Pro Lys Gln Thr Gln Asp Gly Pro Gly Asp Leu	
450 455 460	
ttt tca tca ctt gct tca att ggt att gtc gta gat gct gat gag ggt	1442
Phe Ser Ser Leu Ala Ser Ile Gly Ile Val Val Asp Ala Asp Glu Gly	
465 470 475	
agt gaa act ttt gga caa ctt aaa att tta gat aga gaa aca att ggt	1490

Ser Glu Thr Phe Gly Gln Leu Lys Ile Leu Asp Arg Glu Thr Ile Gly  
 480 485 490  
 cct gat gca cct tat aca act ctt gat gag gca tta aaa aaa gat cca 1538  
 Pro Asp Ala Pro Tyr Thr Thr Leu Asp Glu Ala Leu Lys Lys Asp Pro  
 495 500 505  
 caa gca gta gca gat ata tta gct ggt agt tct gga ata tct gat tca 1586  
 Gln Ala Val Ala Asp Ile Leu Ala Gly Ser Ser Gly Ile Ser Asp Ser  
 510 515 520 525  
 aca gat ttt tct tat caa gat cat att gtt gga aaa aca caa gct ggt 1634  
 Thr Asp Phe Ser Tyr Gln Asp His Ile Val Gly Lys Thr Gln Ala Gly  
 530 535 540  
 aca tat gat gta aag tat tct gta gat gca agt ggt act ata gga gac 1682  
 Thr Tyr Asp Val Lys Tyr Ser Val Asp Ala Ser Gly Thr Ile Gly Asp  
 545 550 555  
 gtt tac att gga ggt gta aaa gct tct cta tct gat cct gca aaa aat 1730  
 Val Tyr Ile Gly Gly Val Lys Ala Ser Leu Ser Asp Pro Ala Lys Asn  
 560 565 570  
 ata tat acg gtc aca tct ggt cct gct aca ggt ctt agt ata gca gtt 1778  
 Ile Tyr Thr Val Thr Ser Gly Pro Ala Thr Gly Leu Ser Ile Ala Val  
 575 580 585  
 aat aat cgt act cca ggt atc aat gta gaa agt act gta aga gtc aaa 1826  
 Asn Asn Arg Thr Pro Gly Ile Asn Val Glu Ser Thr Val Arg Val Lys  
 590 595 600 605  
 caa ggt aaa ctt agc caa ata caa gaa gca ctt aaa gct gaa gta cag 1874  
 Gln Gly Lys Leu Ser Gln Ile Gln Glu Ala Leu Lys Ala Glu Val Gln  
 610 615 620  
 caa gat cct tta aaa gaa aac aca ggt cct tta att atc atg caa gat 1922  
 Gln Asp Pro Leu Lys Glu Asn Thr Gly Pro Leu Ile Ile Met Gln Asp  
 625 630 635  
 aac tat aag gat gtt atg aaa aat ctt gag aca aga ata gaa aaa gaa 1970  
 Asn Tyr Lys Asp Val Met Lys Asn Leu Glu Thr Arg Ile Glu Lys Glu  
 640 645 650  
 aca caa aga gtt act agt tgg gaa cgt atg atg cgt tta aaa ttt tct 2018  
 Thr Gln Arg Val Thr Ser Trp Glu Arg Met Met Arg Leu Lys Phe Ser  
 655 660 665  
 aga ctt gat gct gta tta gca aaa tat aat cag atg atg tca gca aat 2066  
 Arg Leu Asp Ala Val Leu Ala Lys Tyr Asn Gln Met Met Ser Ala Asn  
 670 675 680 685  
 gct tct agt tta ggg caa ctt ggt gca taa 2096  
 Ala Ser Ser Leu Gly Gln Leu Gly Ala  
 690

<210> 10  
 <211> 694  
 <212> PRT  
 <213> Lawsonia intracellularis

<400> 10

Met Ala Asp Tyr Leu Ser Gly Gly Ile Ser Phe Gly Gly Ile Gly Ser  
 1 5 10 15

Gly Thr Asp Phe Gln Ala Met Ile Asp Gln Leu Lys Lys Ile Glu Leu  
 20 25 30

Ile Pro Lys Asn Arg Leu Val Val Ser His Glu Gln Trp Thr Lys Lys  
 35 40 45

Tyr Lys Ala Phe Glu Glu Leu Ile Lys Thr Val Lys Asp Thr Glu Ala  
 50 55 60

Ser Leu Ser Lys Leu Ser Ser Val Gly Ala Ile Leu Lys Lys Glu Gly  
 65 70 75 80

Ser Val Ser Asn Thr Ser Val Ala Ser Val Lys Ala Ser Ser Asp Ala  
 85 90 95

Ser Asp Gly Thr His Thr Ile Asp Val Lys Gln Leu Ala Thr Asn Thr  
 100 105 110

Ile Leu Ser Asn Asn His Ile Phe Asp Ser Lys Thr Glu Ser Ile Asn  
 115 120 125

Asn Thr Gly Ser Pro Gly Ile Phe Ala Tyr Glu Tyr Lys Gly Glu Leu  
 130 135 140

His Glu Val Glu Val Pro Pro Gly Ser Asp Leu Glu Tyr Leu Ala Thr  
 145 150 155 160

Leu Ile Asn Lys Asp Ser Asn Asn Pro Gly Val Lys Ala Asn Leu Ile  
 165 170 175

Lys Thr Gly Asp Gly Tyr Met Phe Ser Leu Glu Gly Thr Glu Thr Gly  
 180 185 190

Ala Asn Ala Thr Leu Ser Ile Ser Asn Lys Thr Thr Leu Pro Asp Phe  
 195 200 205

Lys Ala Ser Val Ala Thr Ser Ser Ala Leu Ala Asn Gly Glu Asp Thr  
 210 215 220

Ile Ile Asn Thr Ser Gly Thr Thr Gln Gln Phe Ser Phe Glu Tyr Asn  
 225 230 235 240

Gly Arg Thr Phe Thr Phe Asp Ile Pro Ser Gly Thr Thr Ala Lys Glu  
 245 250 255

Leu Gln Thr Ala Ile Asn Glu Asn Thr Lys Asn Thr Gly Val Arg Ala  
 260 265 270

Thr Phe Glu Lys His Gly Ser Asp Ile Val Leu Gln Leu Glu Gly Thr  
 275 280 285

Val Pro Asn Gln Gln Val Lys Val Thr Ala Ser Pro Thr Asp Leu Gly  
 290 295 300

Ser Phe Thr Ser Ser Gly Gln Ala Gly Trp Asn Lys Arg Asp Ser Gln  
 305 310 315 320

Asp Ala Ile Phe Asn Ile Asn Gly Trp Asp Gln Glu Leu Thr Ser Ser  
 325 330 335

Thr Asn Glu Leu Thr Glu Val Ile Pro Gly Leu Gln Ile Thr Leu Leu  
 340 345 350

Ser Glu Gly Lys Thr Gln Ile Thr Ile Gln Thr Ser Thr Asp Glu Val  
 355 360 365

Lys Lys Gln Val Glu Lys Ala Val Glu Ser Ile Asn Asn Val Leu Ser  
 370 375 380

Lys Ile Gln Glu Leu Thr Lys Ala Thr Ala Glu Asp Lys Asp Asp Ser  
 385 390 395 400

Lys Asp Thr Ser Ser Ser Ser Ser Lys Ile Pro Ser Tyr Leu Gln Ser  
 405 410 415

Pro Thr Lys Val Lys Ala Gly Leu Phe Thr Gly Asp Thr Gly Ile Gln  
 420 425 430

Met Leu Ser Thr Arg Leu Lys Ser Ile Phe Ser Ser Asn Gly Leu Gly  
 435 440 445

Phe Ser Pro Lys Gln Thr Gln Asp Gly Pro Gly Asp Leu Phe Ser Ser  
 450 455 460

Leu Ala Ser Ile Gly Ile Val Val Asp Ala Asp Glu Gly Ser Glu Thr  
 465 470 475 480

Phe Gly Gln Leu Lys Ile Leu Asp Arg Glu Thr Ile Gly Pro Asp Ala  
 485 490 495

Pro Tyr Thr Thr Leu Asp Glu Ala Leu Lys Lys Asp Pro Gln Ala Val  
 500 505 510

Ala Asp Ile Leu Ala Gly Ser Ser Gly Ile Ser Asp Ser Thr Asp Phe  
 515 520 525

Ser Tyr Gln Asp His Ile Val Gly Lys Thr Gln Ala Gly Thr Tyr Asp  
530 535 540

Val Lys Tyr Ser Val Asp Ala Ser Gly Thr Ile Gly Asp Val Tyr Ile  
545 550 555 560

Gly Gly Val Lys Ala Ser Leu Ser Asp Pro Ala Lys Asn Ile Tyr Thr  
565 570 575

Val Thr Ser Gly Pro Ala Thr Gly Leu Ser Ile Ala Val Asn Asn Arg  
580 585 590

Thr Pro Gly Ile Asn Val Glu Ser Thr Val Arg Val Lys Gln Gly Lys  
595 600 605

Leu Ser Gln Ile Gln Glu Ala Leu Lys Ala Glu Val Gln Gln Asp Pro  
610 615 620

Leu Lys Glu Asn Thr Gly Pro Leu Ile Ile Met Gln Asp Asn Tyr Lys  
625 630 635 640

Asp Val Met Lys Asn Leu Glu Thr Arg Ile Glu Lys Glu Thr Gln Arg  
645 650 655

Val Thr Ser Trp Glu Arg Met Met Arg Leu Lys Phe Ser Arg Leu Asp  
660 665 670

Ala Val Leu Ala Lys Tyr Asn Gln Met Met Ser Ala Asn Ala Ser Ser  
675 680 685

Leu Gly Gln Leu Gly Ala  
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<222> (13)..(1200)

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1 5 10

tcc aca aca aat caa atg acc aat gca gct gct ggt aat act aat aga 99  
Ser Thr Thr Asn Gln Met Thr Asn Ala Ala Ala Gly Asn Thr Asn Arg  
15 20 25

gct acc ggt agt atg aac ggt cgt aat ctc aca caa ata aaa aca cct 147  
Ala Thr Gly Ser Met Asn Gly Arg Asn Leu Thr Gln Ile Lys Thr Pro

30	35	40	45	
cag tcc atg att gat aat gct tca gaa gaa tta aca act tct ctt gaa				195
Gln Ser Met Ile Asp Asn Ala Ser Glu Glu Leu Thr Thr Ser Leu Glu	50	55	60	
tct aaa agc agt gac gac ttt gca att aaa gat cgt aaa aga caa ggg				243
Ser Lys Ser Ser Asp Asp Phe Ala Ile Lys Asp Arg Lys Arg Gln Gly	65	70	75	
aaa gga tct gat tct cta tta aaa atg gtt caa gaa tat aca gag ctg				291
Lys Gly Ser Asp Ser Leu Leu Lys Met Val Gln Glu Tyr Thr Glu Leu	80	85	90	
acg aat gat gat acc cgt aat gct aaa aga gct atg tta tcc cag gta				339
Thr Asn Asp Asp Thr Arg Asn Ala Lys Arg Ala Met Leu Ser Gln Val	95	100	105	
tta cgt gca agt caa agt tca caa gat gta ctc gaa aaa aca tta gaa				387
Leu Arg Ala Ser Gln Ser Ser Gln Asp Val Leu Glu Lys Thr Leu Glu	110	115	120	125
caa ttt tct aat aaa aca gat gct tgg gct tct ctt gca gaa att gca				435
Gln Phe Ser Asn Lys Thr Asp Ala Trp Ala Ser Leu Ala Glu Ile Ala	130	135	140	
caa gaa tat ggt gca gaa tct cca cag cca aca gga tta aaa tct gta				483
Gln Glu Tyr Gly Ala Glu Ser Pro Gln Pro Thr Gly Leu Lys Ser Val	145	150	155	
tta gat gct atg gag aca tta gaa aat gag ttt ggt gat gaa att aaa				531
Leu Asp Ala Met Glu Thr Leu Glu Asn Glu Phe Gly Asp Glu Ile Lys	160	165	170	
gca gga cta aaa gga gct cta aat tca aaa gaa ttt act gat ata ggc				579
Ala Gly Leu Lys Gly Ala Leu Asn Ser Lys Glu Phe Thr Asp Ile Gly	175	180	185	
agt gca gca cag tta aga gat ctt tat aca aca aca gta act ata aca				627
Ser Ala Ala Gln Leu Arg Asp Leu Tyr Thr Thr Thr Val Thr Ile Thr	190	195	200	205
gct gca cct gat gca gtg tta gca aga ctt ctt gaa gaa tat gag agt				675
Ala Ala Pro Asp Ala Val Leu Ala Arg Leu Leu Glu Glu Tyr Glu Ser	210	215	220	
gat gat gat ctg gat aga gcc att gat ttc ctt cta tct aca ctt ggt				723
Asp Asp Asp Leu Asp Arg Ala Ile Asp Phe Leu Leu Ser Thr Leu Gly	225	230	235	
gga gag ctt gaa tca gct gat cca agt atg gat aaa gta cat ctt Caa				771
Gly Glu Leu Glu Ser Ala Asp Pro Ser Met Asp Lys Val His Leu Gln	240	245	250	
agt gta atg ggt gat att gaa aaa aca caa caa ctt cat agc tct cat				819
Ser Val Met Gly Asp Ile Glu Lys Thr Gln Gln Leu His Ser Ser His	255	260	265	
aaa caa tgt act aca gcc ctt agc agg tgg aaa gag aaa cat aaa ggt				867
Lys Gln Cys Thr Thr Ala Leu Ser Arg Trp Lys Glu Lys His Lys Gly	270	275	280	285
ggg ggg gaa aat agt aca cta act cct tta gaa atg atg cgt gaa cta				915
Gly Gly Glu Asn Ser Thr Leu Thr Pro Leu Glu Met Met Arg Glu Leu	290	295	300	



att gca cta aaa aat gaa aat ttt att tct cct tcc tct ata gat aaa 963  
 Ile Ala Leu Lys Asn Glu Asn Phe Ile Ser Pro Ser Ser Ile Asp Lys  
 305 310 315  
 att gtt gat caa gct gat ccc caa gat att gaa aaa gaa gtc ctt ttt 1011  
 Ile Val Asp Gln Ala Asp Pro Gln Asp Ile Glu Lys Glu Val Leu Phe  
 320 325 330  
 tta caa gag atg tta gct gct gta aga aaa ttt ccc att atg gta ttt 1059  
 Leu Gln Glu Met Leu Ala Ala Val Arg Lys Phe Pro Ile Met Val Phe  
 335 340 345  
 gat aat gtc gaa aat cgt gta aga gtt atg ggt gct gta caa gat gct 1107  
 Asp Asn Val Glu Asn Arg Val Arg Val Met Gly Ala Val Gln Asp Ala  
 350 355 360 365  
 gtt gac gat gct gta aga aga gaa gat gaa ttc ctc ttt caa aaa gaa 1155  
 Val Asp Asp Ala Val Arg Arg Glu Asp Glu Phe Leu Phe Gln Lys Glu  
 370 375 380  
 cat cct gat gta cca cta caa cca gat gaa aat aat ata caa taa 1200  
 His Pro Asp Val Pro Leu Gln Pro Asp Glu Asn Asn Ile Gln  
 385 390 395

<210> 12  
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 <212> PRT  
 <213> Lawsonia intracelluláris

<400> 12

Met Ala Asn Val Ser Gly Ile Pro Ala Pro Arg Leu Leu Ser Thr Thr  
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Asn Gln Met Thr Asn Ala Ala Ala Gly Asn Thr Asn Arg Ala Thr Gly  
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35 40 45

Ile Asp Asn Ala Ser Glu Glu Leu Thr Thr Ser Leu Glu Ser Lys Ser  
50 55 60

Ser Asp Asp Phe Ala Ile Lys Asp Arg Lys Arg Gln Gly Lys Gly Ser  
65 70 75 80

Asp Ser Leu Leu Lys Met Val Gln Glu Tyr Thr Glu Leu Thr Asn Asp  
85 90 95

Asp Thr Arg Asn Ala Lys Arg Ala Met Leu Ser Gln Val Leu Arg Ala  
100 105 110

Ser Gln Ser Ser Gln Asp Val Leu Glu Lys Thr Leu Glu Gln Phe Ser  
115 120 125

Asn Lys Thr Asp Ala Trp Ala Ser Leu Ala Glu Ile Ala Gln Glu Tyr  
 130 135 140

Gly Ala Glu Ser Pro Gln Pro Thr Gly Leu Lys Ser Val Leu Asp Ala  
 145 150 155 160

Met Glu Thr Leu Glu Asn Glu Phe Gly Asp Glu Ile Lys Ala Gly Leu  
 165 170 175

Lys Gly Ala Leu Asn Ser Lys Glu Phe Thr Asp Ile Gly Ser Ala Ala  
 180 185 190

Gln Leu Arg Asp Leu Tyr Thr Thr Thr Val Thr Ile Thr Ala Ala Pro  
 195 200 205

Asp Ala Val Leu Ala Arg Leu Leu Glu Glu Tyr Glu Ser Asp Asp Asp  
 210 215 220

Leu Asp Arg Ala Ile Asp Phe Leu Leu Ser Thr Leu Gly Gly Glu Leu  
 225 230 235 240

Glu Ser Ala Asp Pro Ser Met Asp Lys Val His Leu Gln Ser Val Met  
 245 250 255

Gly Asp Ile Glu Lys Thr Gln Gln Leu His Ser Ser His Lys Gln Cys  
 260 265 270

Thr Thr Ala Leu Ser Arg Trp Lys Glu Lys His Lys Gly Gly Gly Glu  
 275 280 285

Asn Ser Thr Leu Thr Pro Leu Glu Met Met Arg Glu Leu Ile Ala Leu  
 290 295 300

Lys Asn Glu Asn Phe Ile Ser Pro Ser Ser Ile Asp Lys Ile Val Asp  
 305 310 315 320

Gln Ala Asp Pro Gln Asp Ile Glu Lys Glu Val Leu Phe Leu Gln Glu  
 325 330 335

Met Leu Ala Ala Val Arg Lys Phe Pro Ile Met Val Phe Asp Asn Val  
 340 345 350

Glu Asn Arg Val Arg Val Met Gly Ala Val Gln Asp Ala Val Asp Asp  
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 370 375 380

Val Pro Leu Gln Pro Asp Glu Asn Asn Ile Gln

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gaa gaa gga ctt gaa gaa ctt gaa ggt ggt gtt cct aaa gag caa ggt 148  
Glu Glu Gly Leu Glu Glu Leu Glu Gly Gly Val Pro Lys Glu Gln Gly  
25 30 35

ggt cca ggt aaa gga gat gct tca gag gct gct aaa ggt caa gca gca 196  
Gly Pro Gly Lys Gly Asp Ala Ser Glu Ala Ala Lys Gly Gln Ala Ala  
40 45 50 55

gca gat agt att aat tca gct ggt ggt act gaa aag cct gga gaa gtt 244  
Ala Asp Ser Ile Asn Ser Ala Gly Gly Thr Glu Lys Pro Gly Glu Val  
60 65 70

ggg gat aag gaa gat gta ggg gaa ggt ggc gaa ata cct gaa ggt ggt 292  
Gly Asp Lys Glu Asp Val Gly Glu Gly Gly Glu Ile Pro Glu Gly Gly  
75 80 85

gaa ata cct gag ggt ggt gaa gaa gtt cca gag gaa ccc cca tat gtc 340  
Glu Ile Pro Glu Gly Gly Glu Glu Val Pro Glu Glu Pro Pro Tyr Val  
90 95 100

cct cct cca ttg gtt gaa cca gct aaa atc agt aca gta aca gat ctc 388  
Pro Pro Pro Leu Val Glu Pro Ala Lys Ile Ser Thr Val Thr Asp Leu  
105 110 115

agt acg tta atg gga tca cta cag ctg aca gag caa aaa aag aat gct 436  
Ser Thr Leu Met Gly Ser Leu Gln Leu Thr Glu Gln Lys Lys Asn Ala  
120 125 130 135

gaa aaa aca gta aat gaa att aaa gca cag aat aaa gag caa caa gta 484  
Glu Lys Thr Val Asn Glu Ile Lys Ala Gln Asn Lys Glu Gln Gln Val  
140 145 150

aag ttc caa gag caa att aaa aag att gag gat aat att gct gaa tct 532  
Lys Phe Gln Glu Gln Ile Lys Lys Ile Glu Asp Asn Ile Ala Glu Ser  
155 160 165

aag aaa agt ggt ata ctt aag ttt ttc caa aag ttg ttt gca gtt att 580  
Lys Lys Ser Gly Ile Leu Lys Phe Phe Gln Lys Leu Phe Ala Val Ile  
170 175 180

ggt gct gta cta gga gct att gga ggt gcg cta gct att gct gca ggt 628  
Gly Ala Val Leu Gly Ala Ile Gly Gly Ala Leu Ala Ile Ala Ala Gly  
185 190 195

gct gct tca ggt aac cca tta ttg gtt gct gca ggt att atg gct att 676  
 Ala Ala Ser Gly Asn Pro Leu Leu Val Ala Ala Gly Ile Met Ala Ile  
 200 205 210 215  
 gta gct tca att gat gca gca atg tct tct cta tct gat ggt aaa gtg 724  
 Val Ala Ser Ile Asp Ala Ala Met Ser Ser Leu Ser Asp Gly Lys Val  
 220 225 230  
 tcc atc tca gca ggg att agt aag gct ctt gag gct atg gga gta cca 772  
 Ser Ile Ser Ala Gly Ile Ser Lys Ala Leu Glu Ala Met Gly Val Pro  
 235 240 245  
 gca gaa aca gca caa tgg att gca ttt ggt ata cag tta gca atg att 820  
 Ala Glu Thr Ala Gln Trp Ile Ala Phe Gly Ile Gln Leu Ala Met Ile  
 250 255 260  
 gca gtg act ata gct att ggt ttt gcc tct ggt ggt ggt gga gca atg 868  
 Ala Val Thr Ile Ala Ile Gly Phe Ala Ser Gly Gly Gly Gly Ala Met  
 265 270 275  
 gct gga gtg tca aaa ata gca gat atg ttt tca aag tct caa gat gta 916  
 Ala Gly Val Ser Lys Ile Ala Asp Met Phe Ser Lys Ser Gln Asp Val  
 280 285 290 295  
 gct aag ttg gca cag atg att gaa aaa gct tct aaa ata gta caa atc 964  
 Ala Lys Leu Ala Gln Met Ile Glu Lys Ala Ser Lys Ile Val Gln Ile  
 300 305 310  
 gct ggt tca gtt aat cag tct gct ata ggc ggt aca ggt att ggt aca 1012  
 Ala Gly Ser Val Asn Gln Ser Ala Ile Gly Gly Thr Gly Ile Gly Thr  
 315 320 325  
 gct gta gtg caa agc aat ata aaa gct aat gaa tct gaa caa aaa gaa 1060  
 Ala Val Val Gln Ser Asn Ile Lys Ala Asn Glu Ser Glu Gln Lys Glu  
 330 335 340  
 att gaa gct gct att gca aaa gtt aaa gct aag ata gag acg tta caa 1108  
 Ile Glu Ala Ala Ile Ala Lys Val Lys Ala Lys Ile Glu Thr Leu Gln  
 345 350 355  
 gac ttc ttt aaa aac caa atg gaa caa ttc aat gct ata atg aaa ata 1156  
 Asp Phe Phe Lys Asn Gln Met Glu Gln Phe Asn Ala Ile Met Lys Ile  
 360 365 370 375  
 ata aca gat att att caa gat agc gtc aat aca aaa ata gct gtt caa 1204  
 Ile Thr Asp Ile Ile Gln Asp Ser Val Asn Thr Lys Ile Ala Val Gln  
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 <213> Lawsonia intracellularis

<400> 14

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 35 40 45  
 Ala Ala Lys Gly Gln Ala Ala Ala Asp Ser Ile Asn Ser Ala Gly Gly  
 50 55 60  
 Thr Glu Lys Pro Gly Glu Val Gly Asp Lys Glu Asp Val Gly Glu Gly  
 65 70 75 80  
 Gly Glu Ile Pro Glu Gly Gly Glu Ile Pro Glu Gly Gly Glu Glu Val  
 85 90 95  
 Pro Glu Glu Pro Pro Tyr Val Pro Pro Pro Leu Val Glu Pro Ala Lys  
 100 105 110  
 Ile Ser Thr Val Thr Asp Leu Ser Thr Leu Met Gly Ser Leu Gln Leu  
 115 120 125  
 Thr Glu Gln Lys Lys Asn Ala Glu Lys Thr Val Asn Glu Ile Lys Ala  
 130 135 140  
 Gln Asn Lys Glu Gln Gln Val Lys Phe Gln Glu Gln Ile Lys Lys Ile  
 145 150 155 160  
 Glu Asp Asn Ile Ala Glu Ser Lys Lys Ser Gly Ile Leu Lys Phe Phe  
 165 170 175  
 Gln Lys Leu Phe Ala Val Ile Gly Ala Val Leu Gly Ala Ile Gly Gly  
 180 185 190  
 Ala Leu Ala Ile Ala Ala Gly Ala Ala Ser Gly Asn Pro Leu Leu Val  
 195 200 205  
 Ala Ala Gly Ile Met Ala Ile Val Ala Ser Ile Asp Ala Ala Met Ser  
 210 215 220  
 Ser Leu Ser Asp Gly Lys Val Ser Ile Ser Ala Gly Ile Ser Lys Ala  
 225 230 235 240  
 Leu Glu Ala Met Gly Val Pro Ala Glu Thr Ala Gln Trp Ile Ala Phe  
 245 250 255  
 Gly Ile Gln Leu Ala Met Ile Ala Val Thr Ile Ala Ile Gly Phe Ala  
 260 265 270

Ser Gly Gly Gly Gly Ala Met Ala Gly Val Ser Lys Ile Ala Asp Met  
275 280 285

Phe Ser Lys Ser Gln Asp Val Ala Lys Leu Ala Gln Met Ile Glu Lys  
290 295 300

Ala Ser Lys Ile Val Gln Ile Ala Gly Ser Val Asn Gln Ser Ala Ile  
305 310 315 320

Gly Gly Thr Gly Ile Gly Thr Ala Val Val Gln Ser Asn Ile Lys Ala  
325 330 335

Asn Glu Ser Glu Gln Lys Glu Ile Glu Ala Ala Ile Ala Lys Val Lys  
340 345 350

Ala Lys Ile Glu Thr Leu Gln Asp Phe Phe Lys Asn Gln Met Glu Gln  
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Phe Asn Ala Ile Met Lys Ile Ile Thr Asp Ile Ile Gln Asp Ser Val  
370 375 380

Asn Thr Lys Ile Ala Val Gln Arg Gly Ala Arg Glu  
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<222> (13)..(894)

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gct caa cgt aac tta agc aag tct tat gga gaa ctg agt tct tct gtt 99  
Ala Gln Arg Asn Leu Ser Lys Ser Tyr Gly Glu Leu Ser Ser Ser Val  
15 20 25

cga aaa ctt tct tca ggt ctt cgt gta gga act gct gct gat gac tca 147  
Arg Lys Leu Ser Ser Gly Leu Arg Val Gly Thr Ala Ala Asp Asp Ser  
30 35 40 45

gca ggg tta gcc att cga gaa ctc atg aga tct gac att gca aca aca 195  
Ala Gly Leu Ala Ile Arg Glu Leu Met Arg Ser Asp Ile Ala Thr Thr  
50 55 60

caa caa gga ata cga aat gcg aat gat gct att tct atg att caa act 243  
Gln Gln Gly Ile Arg Asn Ala Asn Asp Ala Ile Ser Met Ile Gln Thr  
65 70 75

gcg gat ggt gca ctt gga gtc atc gat gaa aag ctc att cga atg aaa 291

Ala Asp Gly Ala Leu Gly Val	Ile Asp Glu Lys Leu Ile Arg Met Lys	
80	85	90
gaa ctt gct gaa caa gct gct aca ggt aca tat aac tcc act cag cgt		339
Glu Leu Ala Glu Gln Ala Ala Thr Gly Thr Tyr Asn Ser Thr Gln Arg		
95	100	105
atg att att gac tct gaa tat caa gct atg gcc tca gaa att act cgt		387
Met Ile Ile Asp Ser Glu Tyr Gln Ala Met Ala Ser Glu Ile Thr Arg		
110	115	120
att gct aat gcg aca gaa ttt aat ggt ata aaa ctt ctt gat ggt tca		435
Ile Ala Asn Ala Thr Glu Phe Asn Gly Ile Lys Leu Leu Asp Gly Ser		
	130	135
tta tca ggt aat cat gat ggg aaa aaa ata aat tca act ggt gca gta		483
Leu Ser Gly Asn His Asp Gly Lys Lys Ile Asn Ser Thr Gly Ala Val		
	145	150
cgt atc cac ttt ggg aca tct aac agc tct gct gaa gat tac tat gat		531
Arg Ile His Phe Gly Thr Ser Asn Ser Ser Ala Glu Asp Tyr Tyr Asp		
	160	165
att aaa att ggt ggc tct aca gct tct gca tta gga ctt ggt aat aca		579
Ile Lys Ile Gly Gly Ser Thr Ala Ser Ala Leu Gly Leu Gly Asn Thr		
	175	180
gta aaa ggt gcg ggt gct aca gtc tct act caa gct gca gca caa aat		627
Val Lys Gly Ala Gly Ala Thr Val Ser Thr Gln Ala Ala Ala Gln Asn		
190	195	200
gcc tta aaa gct ata gat aat gcc att gtt tca aaa gat aaa att cga		675
Ala Leu Lys Ala Ile Asp Asn Ala Ile Val Ser Lys Asp Lys Ile Arg		
	210	215
gca cac ctt ggt gga tta caa aat aga ctt gaa gct aca gtt gat aat		723
Ala His Leu Gly Gly Leu Gln Asn Arg Leu Glu Ala Thr Val Asp Asn		
	225	230
tta agt ata caa aat gaa aac tta caa gct gct gaa tct cgt ata tct		771
Leu Ser Ile Gln Asn Glu Asn Leu Gln Ala Ala Glu Ser Arg Ile Ser		
	240	245
gat ata gat gta agc caa gaa atg aca caa ttt gta cgt aac caa ata		819
Asp Ile Asp Val Ser Gln Glu Met Thr Gln Phe Val Arg Asn Gln Ile		
	255	260
ctt aca caa aca ggt gtt gct atg ctt tca caa gct aat tct cta cca		867
Leu Thr Gln Thr Gly Val Ala Met Leu Ser Gln Ala Asn Ser Leu Pro		
270	275	280
cgt atg gct cag caa ctt att ggc taa		894
Arg Met Ala Gln Gln Leu Ile Gly		
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&lt;210&gt; 16

&lt;211&gt; 293

&lt;212&gt; PRT

&lt;213&gt; Lawsonia intracellularis

&lt;400&gt; 16

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Asn Leu Ser Lys Ser Tyr Gly Glu Leu Ser Ser Ser Val Arg Lys Leu  
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 Ser Ser Gly Leu Arg Val Gly Thr Ala Ala Asp Asp Ser Ala Gly Leu  
 35 40 45  
 Ala Ile Arg Glu Leu Met Arg Ser Asp Ile Ala Thr Thr Gln Gln Gly  
 50 55 60  
 Ile Arg Asn Ala Asn Asp Ala Ile Ser Met Ile Gln Thr Ala Asp Gly  
 65 70 75 80  
 Ala Leu Gly Val Ile Asp Glu Lys Leu Ile Arg Met Lys Glu Leu Ala  
 85 90 95  
 Glu Gln Ala Ala Thr Gly Thr Tyr Asn Ser Thr Gln Arg Met Ile Ile  
 100 105 110  
 Asp Ser Glu Tyr Gln Ala Met Ala Ser Glu Ile Thr Arg Ile Ala Asn  
 115 120 125  
 Ala Thr Glu Phe Asn Gly Ile Lys Leu Leu Asp Gly Ser Leu Ser Gly  
 130 135 140  
 Asn His Asp Gly Lys Lys Ile Asn Ser Thr Gly Ala Val Arg Ile His  
 145 150 155 160  
 Phe Gly Thr Ser Asn Ser Ser Ala Glu Asp Tyr Tyr Asp Ile Lys Ile  
 165 170 175  
 Gly Gly Ser Thr Ala Ser Ala Leu Gly Leu Gly Asn Thr Val Lys Gly  
 180 185 190  
 Ala Gly Ala Thr Val Ser Thr Gln Ala Ala Ala Gln Asn Ala Leu Lys  
 195 200 205  
 Ala Ile Asp Asn Ala Ile Val Ser Lys Asp Lys Ile Arg Ala His Leu  
 210 215 220  
 Gly Gly Leu Gln Asn Arg Leu Glu Ala Thr Val Asp Asn Leu Ser Ile  
 225 230 235 240  
 Gln Asn Glu Asn Leu Gln Ala Ala Glu Ser Arg Ile Ser Asp Ile Asp  
 245 250 255  
 Val Ser Gln Glu Met Thr Gln Phe Val Arg Asn Gln Ile Leu Thr Gln  
 260 265 270



Thr Gly Val Ala Met Leu Ser Gln Ala Asn Ser Leu Pro Arg Met Ala  
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Gln Gln Leu Ile Gly  
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<210> 17  
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 Gln Ile Ile Lys Ile Leu Leu Phe Ser Leu Cys Val Phe Phe Phe Thr  
 10 15 20

ctt aca gaa aaa caa aaa att tat gct gca gac gtc ttt ttt gag ggc 148  
 Leu Thr Glu Lys Gln Lys Ile Tyr Ala Ala Asp Val Phe Phe Glu Gly  
 25 30 35 40

aga acc gaa acc tta atc aat gta aac aaa cca ttt gat tct ttt ttt 196  
 Arg Thr Glu Thr Leu Ile Asn Val Asn Lys Pro Phe Asp Ser Phe Phe  
 45 50 55

gga ggt tct gac tct aca ata gga acc ctt gaa aca gga cct act aat 244  
 Gly Gly Ser Asp Ser Thr Ile Gly Thr Leu Glu Thr Gly Pro Thr Asn  
 60 65 70

ctt acc ttc aca aca gta gga gcc ttc cgc aat tct gtt ttc aga att 292  
 Leu Thr Phe Thr Thr Val Gly Ala Phe Arg Asn Ser Val Phe Arg Ile  
 75 80 85

att ggt ggt ggt agg tct agt ttt aac aac cca aat aca gtt aaa ggc 340  
 Ile Gly Gly Gly Arg Ser Ser Phe Asn Asn Pro Asn Thr Val Lys Gly  
 90 95 100

aat gtt act cta act gtt tat aat act gat gta gaa aga ata att ggt 388  
 Asn Val Thr Leu Thr Val Tyr Asn Thr Asp Val Glu Arg Ile Ile Gly  
 105 110 115 120

gca ggt atc agc aat aga gga ctt gta acc gtt act ggc tca gta aat 436  
 Ala Gly Ile Ser Asn Arg Gly Leu Val Thr Val Thr Gly Ser Val Asn  
 125 130 135

atg aag cta gaa aat gtt tct gtt act aga gga att tat ggt ggt gtc 484  
 Met Lys Leu Glu Asn Val Ser Val Thr Arg Gly Ile Tyr Gly Gly Val  
 140 145 150

tat act caa aat gga cat gta cta ggc tct atc aac atg cat ttg aaa 532  
 Tyr Thr Gln Asn Gly His Val Leu Gly Ser Ile Asn Met His Leu Lys  
 155 160 165

aac gtc caa act cca cta tta ata ggt tct gga gta agc aat gga cct 580

Asn	Val	Gln	Thr	Pro	Leu	Leu	Ile	Gly	Ser	Gly	Val	Ser	Asn	Gly	Pro	
170						175					180					
aat	cgt	att	act	gta	aat	gga	gac	ata	aac	att	gat	gtt	gaa	gac	tct	628
Asn	Arg	Ile	Thr	Val	Asn	Gly	Asp	Ile	Asn	Ile	Asp	Val	Glu	Asp	Ser	
185					190					195					200	
agg	att	caa	tat	gta	aac	att	aca	gga	gaa	gta	gat	gca	ggg	ata	aaa	676
Arg	Ile	Gln	Tyr	Val	Asn	Ile	Thr	Gly	Glu	Val	Asp	Ala	Gly	Ile	Lys	
				205				210						215		
gga	aat	gct	act	cta	act	gta	aaa	aaa	tct	act	gtt	gag	ctt	ata	aac	724
Gly	Asn	Ala	Thr	Leu	Thr	Val	Lys	Lys	Ser	Thr	Val	Glu	Leu	Ile	Asn	
			220					225					230			
tct	ggt	aga	ggt	aat	atc	tta	ggt	aat	ctc	aaa	ata	tct	ata	gca	gat	772
Ser	Gly	Arg	Gly	Asn	Ile	Leu	Gly	Asn	Leu	Lys	Ile	Ser	Ile	Ala	Asp	
		235					240					245				
tca	aat	ata	agg	ggg	tta	tca	cca	gta	gac	ttt	ggt	tct	tca	gta	tat	820
Ser	Asn	Ile	Arg	Gly	Leu	Ser	Pro	Val	Asp	Phe	Gly	Ser	Ser	Val	Tyr	
	250					255					260					
ggg	gac	aca	tct	ata	aat	gta	att	aat	tct	cag	att	aat	gat	att	act	868
Gly	Asp	Thr	Ser	Ile	Asn	Val	Ile	Asn	Ser	Gln	Ile	Asn	Asp	Ile	Thr	
265					270					275					280	
ctt	ata	cca	agg	gct	ggt	gga	atg	ctt	gta	ggt	cct	gtt	acc	cta	gat	916
Leu	Ile	Pro	Arg	Ala	Gly	Gly	Met	Leu	Val	Gly	Pro	Val	Thr	Leu	Asp	
				285					290					295		
atc	aca	agc	agt	act	ata	caa	aat	ata	caa	tgt	ggg	cct	gtc	agt	caa	964
Ile	Thr	Ser	Ser	Thr	Ile	Gln	Asn	Ile	Gln	Cys	Gly	Pro	Val	Ser	Gln	
			300					305					310			
aat	aat	caa	ctt	aac	aca	cta	aat	gta	act	gtt	aat	act	agt	aac	att	1012
Asn	Asn	Gln	Leu	Asn	Thr	Leu	Asn	Val	Thr	Val	Asn	Thr	Ser	Asn	Ile	
		315						320				325				
act	aac	tta	aac	ctt	ggt	agt	gtc	gaa	ggt	cat	aca	ata	tca	act	aca	1060
Thr	Asn	Leu	Asn	Leu	Gly	Ser	Val	Glu	Gly	His	Thr	Ile	Ser	Thr	Thr	
	330					335					340					
gca	act	gtt	act	gat	agt	aat	att	act	aac	ctt	aat	gtc	gga	acc	ttc	1108
Ala	Thr	Val	Thr	Asp	Ser	Asn	Ile	Thr	Asn	Leu	Asn	Val	Gly	Thr	Phe	
345					350					355					360	
aat	gga	ctt	gga	gta	act	gag	aat	gcc	tct	gta	atc	att	aat	agt	ggc	1156
Asn	Gly	Leu	Gly	Val	Thr	Glu	Asn	Ala	Ser	Val	Ile	Ile	Asn	Ser	Gly	
				365					370					375		
aat	att	act	aac	ctt	aat	gtc	gga	act	aat	gta	ata	gct	gca	gcc	aca	1204
Asn	Ile	Thr	Asn	Leu	Asn	Val	Gly	Thr	Asn	Val	Ile	Ala	Ala	Ala	Thr	
			380					385					390			
act	att	aat	tcc	tct	gcg	acc	ata	cac	gac	gga	ctt	att	gca	aac	ctt	1252
Thr	Ile	Asn	Ser	Ser	Ala	Thr	Ile	His	Asp	Gly	Leu	Ile	Ala	Asn	Leu	
		395					400					405				
acc	tta	ggc	tca	caa	ggt	aat	ggt	cgt	act	atg	ata	gct	aca	gca	aat	1300
Thr	Leu	Gly	Ser	Gln	Gly	Asn	Gly	Arg	Thr	Met	Ile	Ala	Thr	Ala	Asn	
	410					415					420					
gtt	aat	ggt	gga	act	att	gga	tta	tta	act	atg	ggt	tca	gaa	aac	ttc	1348
Val	Asn	Gly	Gly	Thr	Ile	Gly	Leu	Leu	Thr	Met	Gly	Ser	Glu	Asn	Phe	

425	430	435	440	
ata cca ggc aca aga cca att act gaa tta gca ata cta aac atg tct				1396
Ile Pro Gly Thr Arg Pro Ile Thr Glu Leu Ala Ile Leu Asn Met Ser	445	450	455	
ggg gga tta att gaa aga att atc gta ggt aat gcc aac tct tca acc				1444
Gly Gly Leu Ile Glu Arg Ile Ile Val Gly Asn Ala Asn Ser Ser Thr	460	465	470	
ata aac ttt act cct ggg aag aga tca att gta aaa aca ata aat ggt				1492
Ile Asn Phe Thr Pro Gly Lys Arg Ser Ile Val Lys Thr Ile Asn Gly	475	480	485	
cca gaa ctt cca tat tta gtt aac ata caa aaa ggt gct atg aca caa				1540
Pro Glu Leu Pro Tyr Leu Val Asn Ile Gln Lys Gly Ala Met Thr Gln	490	495	500	
tgg ggc act aaa aat atg ccc ttt tta ttg gat aca aga aat tta atc				1588
Trp Gly Thr Lys Asn Met Pro Phe Leu Leu Asp Thr Arg Asn Leu Ile	505	510	515	520
ttg tcc gga act ctg att acc tca aat att caa cta gct gat tta tct				1636
Leu Ser Gly Thr Leu Ile Thr Ser Asn Ile Gln Leu Ala Asp Leu Ser	525	530	535	
ata acc aat cta ttt gtt gct aat ggc ggt aca cta gta cct aga aaa				1684
Ile Thr Asn Leu Phe Val Ala Asn Gly Gly Thr Leu Val Pro Arg Lys	540	545	550	
tta ata cct ggg aac caa cct gtt ata cag ttt ctt gga ggt cct caa				1732
Leu Ile Pro Gly Asn Gln Pro Val Ile Gln Phe Leu Gly Gly Pro Gln	555	560	565	
tca ctc tta gtt atc cat caa cca tta aaa gta aat tta agc tta tca				1780
Ser Leu Leu Val Ile His Gln Pro Leu Lys Val Asn Leu Ser Leu Ser	570	575	580	
cca aaa ctt att gga agt agc atg gtg cca ctt gct ttt gtc tct caa				1828
Pro Lys Leu Ile Gly Ser Ser Met Val Pro Leu Ala Phe Val Ser Gln	585	590	595	600
tct ttt tca tca cca gat ctt ttt gtt aaa caa act aga agt ggt ctc				1876
Ser Phe Ser Ser Pro Asp Leu Phe Val Lys Gln Thr Arg Ser Gly Leu	605	610	615	
att tgg agt gat ctt gag ttt gat cca aca aca tct att tgg tat gtt				1924
Ile Trp Ser Asp Leu Glu Phe Asp Pro Thr Thr Ser Ile Trp Tyr Val	620	625	630	
aat aat atc caa gca tct caa gat ttt tac tct ttc tct att gct cgt				1972
Asn Asn Ile Gln Ala Ser Gln Asp Phe Tyr Ser Phe Ser Ile Ala Arg	635	640	645	
gag act act aac tgg cta aga caa caa cat ata tgg act cta caa aac				2020
Glu Thr Thr Asn Trp Leu Arg Gln Gln His Ile Trp Thr Leu Gln Asn	650	655	660	
cgt tca agt aaa ctt tta gac aac gaa cat tat gga cta tgg ata aat				2068
Arg Ser Ser Lys Leu Leu Asp Asn Glu His Tyr Gly Leu Trp Ile Asn	665	670	675	680
ggt caa ggt gga cat gaa agt ctt gat act tct att ggt agc aaa gca				2116
Val Gln Gly Gly His Glu Ser Leu Asp Thr Ser Ile Gly Ser Lys Ala	685	690	695	

aaa atg cca tgg ata atg gca aca gca gga tat gac tat ctt caa caa Lys Met Pro Trp Ile Met Ala Thr Ala Gly Tyr Asp Tyr Leu Gln Gln 700 705 710	2164
cta cca agg tta gat atg aaa gcc ctt tat ggt ctt gct ttt ggt gct Leu Pro Arg Leu Asp Met Lys Ala Leu Tyr Gly Leu Ala Phe Gly Ala 715 720 725	2212
tct aaa ggt aaa agt aaa tgg tct agc gtc aac tct aca aaa aat gat Ser Lys Gly Lys Ser Lys Trp Ser Ser Val Asn Ser Thr Lys Asn Asp 730 735 740	2260
gct gag cta ggt atg gtt agt ggt tat gta ggt ctt atc cat aac aaa Ala Glu Leu Gly Met Val Ser Gly Tyr Val Gly Leu Ile His Asn Lys 745 750 755 760	2308
act ggg ctc tat agt aca ttg acc tta caa ctt gcg tct agt aaa tta Thr Gly Leu Tyr Ser Thr Leu Thr Leu Gln Leu Ala Ser Ser Lys Leu 765 770 775	2356
cat act aat tct aca ggg ttc tat aga aat ttt aaa tgg aca gaa aca His Thr Asn Ser Thr Gly Phe Tyr Arg Asn Phe Lys Trp Thr Glu Thr 780 785 790	2404
act cca aca gaa gca ctt gaa ctt gga tgg aaa tac act ttc aac aac Thr Pro Thr Glu Ala Leu Glu Leu Gly Trp Lys Tyr Thr Phe Asn Asn 795 800 805	2452
ggt att aaa atg aat cct cgt gga caa ctt att ttt gaa caa aca tct Gly Ile Lys Met Asn Pro Arg Gly Gln Leu Ile Phe Glu Gln Thr Ser 810 815 820	2500
aaa cac cat ttt gat tta gga att caa aat gat aag gct ata tta gat Lys His His Phe Asp Leu Gly Ile Gln Asn Asp Lys Ala Ile Leu Asp 825 830 835 840	2548
aaa agc cag tta ata aca agt tct ctt ggt att acc gtt gaa tat aag Lys Ser Gln Leu Ile Thr Ser Ser Leu Gly Ile Thr Val Glu Tyr Lys 845 850 855	2596
cta cca gtt acc aca cct att aat ctt tat gct ggt att gaa agg ata Leu Pro Val Thr Thr Pro Ile Asn Leu Tyr Ala Gly Ile Glu Arg Ile 860 865 870	2644
aaa ggt cag tct gga aac ttt gca att agt tcc cag agc ctt caa atg Lys Gly Gln Ser Gly Asn Phe Ala Ile Ser Ser Gln Ser Leu Gln Met 875 880 885	2692
aag ttc aag cat gac aat gat aca agt gta gtt aga gca aca ata ggt Lys Phe Lys His Asp Asn Asp Thr Ser Val Val Arg Ala Thr Ile Gly 890 895 900	2740
aca aat ata tta ttg gga gaa cat ttt aat att cac tgt gat ata ttt Thr Asn Ile Leu Leu Gly Glu His Phe Asn Ile His Cys Asp Ile Phe 905 910 915 920	2788
gga gat aaa gga aat gat aaa ggc att ggt ggg caa gca gga ttt aca Gly Asp Lys Gly Asn Asp Lys Gly Ile Gly Gly Gln Ala Gly Phe Thr 925 930 935	2836
tac aaa ttt taa Tyr Lys Phe	2848

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Met Tyr Asn Ile Ile Asn Lys His Gln Ile Ile Lys Ile Leu Leu Phe  
 1 5 10 15

Ser Leu Cys Val Phe Phe Phe Thr Leu Thr Glu Lys Gln Lys Ile Tyr  
 20 25 30

Ala Ala Asp Val Phe Phe Glu Gly Arg Thr Glu Thr Leu Ile Asn Val  
 35 40 45

Asn Lys Pro Phe Asp Ser Phe Phe Gly Gly Ser Asp Ser Thr Ile Gly  
 50 55 60

Thr Leu Glu Thr Gly Pro Thr Asn Leu Thr Phe Thr Thr Val Gly Ala  
 65 70 75 80

Phe Arg Asn Ser Val Phe Arg Ile Ile Gly Gly Gly Arg Ser Ser Phe  
 85 90 95

Asn Asn Pro Asn Thr Val Lys Gly Asn Val Thr Leu Thr Val Tyr Asn  
 100 105 110

Thr Asp Val Glu Arg Ile Ile Gly Ala Gly Ile Ser Asn Arg Gly Leu  
 115 120 125

Val Thr Val Thr Gly Ser Val Asn Met Lys Leu Glu Asn Val Ser Val  
 130 135 140

Thr Arg Gly Ile Tyr Gly Gly Val Tyr Thr Gln Asn Gly His Val Leu  
 145 150 155 160

Gly Ser Ile Asn Met His Leu Lys Asn Val Gln Thr Pro Leu Leu Ile  
 165 170 175

Gly Ser Gly Val Ser Asn Gly Pro Asn Arg Ile Thr Val Asn Gly Asp  
 180 185 190

Ile Asn Ile Asp Val Glu Asp Ser Arg Ile Gln Tyr Val Asn Ile Thr  
 195 200 205

Gly Glu Val Asp Ala Gly Ile Lys Gly Asn Ala Thr Leu Thr Val Lys  
 210 215 220

Lys Ser Thr Val Glu Leu Ile Asn Ser Gly Arg Gly Asn Ile Leu Gly

225		230		235		240									
Asn	Leu	Lys	Ile	Ser	Ile	Ala	Asp	Ser	Asn	Ile	Arg	Gly	Leu	Ser	Pro
				245					250					255	
Val	Asp	Phe	Gly	Ser	Ser	Val	Tyr	Gly	Asp	Thr	Ser	Ile	Asn	Val	Ile
			260					265					270		
Asn	Ser	Gln	Ile	Asn	Asp	Ile	Thr	Leu	Ile	Pro	Arg	Ala	Gly	Gly	Met
		275					280					285			
Leu	Val	Gly	Pro	Val	Thr	Leu	Asp	Ile	Thr	Ser	Ser	Thr	Ile	Gln	Asn
	290					295					300				
Ile	Gln	Cys	Gly	Pro	Val	Ser	Gln	Asn	Asn	Gln	Leu	Asn	Thr	Leu	Asn
305					310					315					320
Val	Thr	Val	Asn	Thr	Ser	Asn	Ile	Thr	Asn	Leu	Asn	Leu	Gly	Ser	Val
			325						330					335	
Glu	Gly	His	Thr	Ile	Ser	Thr	Thr	Ala	Thr	Val	Thr	Asp	Ser	Asn	Ile
			340					345					350		
Thr	Asn	Leu	Asn	Val	Gly	Thr	Phe	Asn	Gly	Leu	Gly	Val	Thr	Glu	Asn
		355					360					365			
Ala	Ser	Val	Ile	Ile	Asn	Ser	Gly	Asn	Ile	Thr	Asn	Leu	Asn	Val	Gly
		370				375					380				
Thr	Asn	Val	Ile	Ala	Ala	Ala	Thr	Thr	Ile	Asn	Ser	Ser	Ala	Thr	Ile
385				390						395					400
His	Asp	Gly	Leu	Ile	Ala	Asn	Leu	Thr	Leu	Gly	Ser	Gln	Gly	Asn	Gly
			405						410					415	
Arg	Thr	Met	Ile	Ala	Thr	Ala	Asn	Val	Asn	Gly	Gly	Thr	Ile	Gly	Leu
			420					425					430		
Leu	Thr	Met	Gly	Ser	Glu	Asn	Phe	Ile	Pro	Gly	Thr	Arg	Pro	Ile	Thr
		435					440					445			
Glu	Leu	Ala	Ile	Leu	Asn	Met	Ser	Gly	Gly	Leu	Ile	Glu	Arg	Ile	Ile
		450				455					460				
Val	Gly	Asn	Ala	Asn	Ser	Ser	Thr	Ile	Asn	Phe	Thr	Pro	Gly	Lys	Arg
465					470					475					480
Ser	Ile	Val	Lys	Thr	Ile	Asn	Gly	Pro	Glu	Leu	Pro	Tyr	Leu	Val	Asn
				485					490					495	

Ile Gln Lys Gly Ala Met Thr Gln Trp Gly Thr Lys Asn Met Pro Phe  
 500 505 510

Leu Leu Asp Thr Arg Asn Leu Ile Leu Ser Gly Thr Leu Ile Thr Ser  
 515 520 525

Asn Ile Gln Leu Ala Asp Leu Ser Ile Thr Asn Leu Phe Val Ala Asn  
 530 535 540

Gly Gly Thr Leu Val Pro Arg Lys Leu Ile Pro Gly Asn Gln Pro Val  
 545 550 555 560

Ile Gln Phe Leu Gly Gly Pro Gln Ser Leu Leu Val Ile His Gln Pro  
 565 570 575

Leu Lys Val Asn Leu Ser Leu Ser Pro Lys Leu Ile Gly Ser Ser Met  
 580 585 590

Val Pro Leu Ala Phe Val Ser Gln Ser Phe Ser Ser Pro Asp Leu Phe  
 595 600 605

Val Lys Gln Thr Arg Ser Gly Leu Ile Trp Ser Asp Leu Glu Phe Asp  
 610 615 620

Pro Thr Thr Ser Ile Trp Tyr Val Asn Asn Ile Gln Ala Ser Gln Asp  
 625 630 635 640

Phe Tyr Ser Phe Ser Ile Ala Arg Glu Thr Thr Asn Trp Leu Arg Gln  
 645 650 655

Gln His Ile Trp Thr Leu Gln Asn Arg Ser Ser Lys Leu Leu Asp Asn  
 660 665 670

Glu His Tyr Gly Leu Trp Ile Asn Val Gln Gly Gly His Glu Ser Leu  
 675 680 685

Asp Thr Ser Ile Gly Ser Lys Ala Lys Met Pro Trp Ile Met Ala Thr  
 690 695 700

Ala Gly Tyr Asp Tyr Leu Gln Gln Leu Pro Arg Leu Asp Met Lys Ala  
 705 710 715 720

Leu Tyr Gly Leu Ala Phe Gly Ala Ser Lys Gly Lys Ser Lys Trp Ser  
 725 730 735

Ser Val Asn Ser Thr Lys Asn Asp Ala Glu Leu Gly Met Val Ser Gly  
 740 745 750

Tyr Val Gly Leu Ile His Asn Lys Thr Gly Leu Tyr Ser Thr Leu Thr  
755 760 765

Leu Gln Leu Ala Ser Ser Lys Leu His Thr Asn Ser Thr Gly Phe Tyr  
770 775 780

Arg Asn Phe Lys Trp Thr Glu Thr Thr Pro Thr Glu Ala Leu Glu Leu  
785 790 795 800

Gly Trp Lys Tyr Thr Phe Asn Asn Gly Ile Lys Met Asn Pro Arg Gly  
805 810 815

Gln Leu Ile Phe Glu Gln Thr Ser Lys His His Phe Asp Leu Gly Ile  
820 825 830

Gln Asn Asp Lys Ala Ile Leu Asp Lys Ser Gln Leu Ile Thr Ser Ser  
835 840 845

Leu Gly Ile Thr Val Glu Tyr Lys Leu Pro Val Thr Thr Pro Ile Asn  
850 855 860

Leu Tyr Ala Gly Ile Glu Arg Ile Lys Gly Gln Ser Gly Asn Phe Ala  
865 870 875 880

Ile Ser Ser Gln Ser Leu Gln Met Lys Phe Lys His Asp Asn Asp Thr  
885 890 895

Ser Val Val Arg Ala Thr Ile Gly Thr Asn Ile Leu Leu Gly Glu His  
900 905 910

Phe Asn Ile His Cys Asp Ile Phe Gly Asp Lys Gly Asn Asp Lys Gly  
915 920 925

Ile Gly Gly Gln Ala Gly Phe Thr Tyr Lys Phe  
930 935